

In the Claims:

Cancel claims 70-76, 82, 83, 89, 94-96, 98-104, and 107-109 without prejudice.

Add new claims 113-192 reading as follows:

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--113. ~~An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to one or more of Q298, G299, G301, Y302, L307, F343, F403, H405, H406, D407, L427, I428, D430, G433, and G475 in Bacillus licheniformis.--~~

--114. The alpha-amylase according to claim 113, wherein said alpha- amylase is produced by Bacillus.--

--115. The alpha-amylase according to claim 114, wherein said alpha- amylase is produced by Bacillus licheniformis, Bacillus amyloliquefaciens or Bacillus stearothermophilus.--

--116. A detergent comprising the alpha-amylase according to claim 113.--

--117. A starch liquefaction composition comprising the alpha-amylase according to claim 113.--

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--118. The alpha-amylase according to claim 113, wherein said alpha- amylase further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in Bacillus licheniformis.--

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--119. The alpha-amylase according to claim 113, wherein said alpha-amylase comprises a substitution or deletion at one or more residues equivalent to M15, V128, H133, N188, A209, and/or M197 in Bacillus licheniformis.--

--120. The alpha-amylase according to claim 113 which is modified by substituting an amino acid residue at a position corresponding to one or more of G301, H405 and/or K406 in Bacillus licheniformis.--

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--121. An alpha-amylase comprising an A domain, a C domain and a calcium binding site, wherein said calcium binding site is associated with said A domain and said C domain and comprises ligand residues in said A domain and/or said C domain, wherein said alpha-amylase is modified to alter the characteristics of said calcium binding site and thereby alter the performance of said alpha-amylase by substituting an amino acid residue at a position corresponding to one or more of Q298, G299, G301, Y302, L307, F343, H405, H406, D407, I428, D430, and G475 in *Bacillus licheniformis*.--

--122. The alpha-amylase according to claim 121, wherein said alpha-amylase is produced by *Bacillus*.--

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--123. The alpha-amylase according to claim 122, wherein said alpha-amylase is produced by *Bacillus licheniformis*, *Bacillus amyloliquefaciens* or *Bacillus stearothermophilus*.--

--124. A detergent comprising the alpha-amylase according to claim 121.--

--125. A starch liquefaction composition comprising the alpha-amylase according to claim 121.--

--126. The alpha-amylase according to claim 121, wherein said alpha-amylase further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis*.--

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--127. The alpha-amylase according to claim 121, wherein said alpha- amylase further comprises a substitution or deletion at one or more residues equivalent to M15, V128, H133, N188, A209, and/or M197 in *Bacillus licheniformis*.--

D' cont.
--128. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and
wherein, in said variant, at least one amino acid residue at a position corresponding to one or more of, Q298, G299, G301, Y302, L307, F343, F403, H405, H406, D407, L427, I428, D430, G433, and G475 in *Bacillus licheniformis* has been substituted.--

--129. The variant according to claim 128, wherein said alpha-amylase is produced by *Bacillus*.--

--130. The variant according to claim 129, wherein said alpha-amylase is produced by *Bacillus licheniformis*, *Bacillus amyloliquefaciens* or *Bacillus stearothermophilus*.--

--131. A detergent comprising the variant according to claim 128.--

--132. A starch liquefaction composition comprising the variant according to claim 128.--

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--133. The variant according to claim 128, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis*.--

--134. The variant according to claim 128, wherein said variant further comprises a substitution or deletion at one or more residue equivalent to M15, V128, H133, N188, A209, and/or M197 in *Bacillus licheniformis*.--

--135. The variant according to claim 128, wherein said variant further comprises a substitution at an amino acid residue at a position corresponding to one or more of G301, H405 and/or K406 in *Bacillus licheniformis*.--

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--136. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, at least one amino acid residue at a position corresponding to one or more of Q298, G299, G301, Y302, L307, F343, H405, H406, D407, I428, D430, and G475 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--137. The variant according to claim 136, wherein said alpha-amylase is produced by *Bacillus*.--

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--138. The variant according to claim 137, wherein said alpha-amylase is produced by *Bacillus licheniformis*, *Bacillus amyloliquefaciens* or *Bacillus stearothermophilus*.--

--139. A detergent comprising the variant according to claim 136.--

--140. A starch liquefaction composition comprising the variant according to claim 136.--

--141. The variant according to claim 136, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis* alpha-amylase.--

--142. The variant according to claim 136, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, V128, H133, N188, A209, and/or M197 in *Bacillus licheniformis* alpha-amylase.--

--143. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and
wherein, in said variant, the amino acid residue at a position corresponding to Q298 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--144. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID

Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and
wherein, in said variant, the amino acid residue at a position corresponding to G299 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--145. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and
wherein, in said variant, the amino acid residue at a position corresponding to G301 in *Bacillus licheniformis* alpha-amylase has been substituted.--

-- 146. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and
wherein, in said variant, the amino acid residue at a position corresponding to Y302 in *Bacillus licheniformis* alpha-amylase has been substituted.--

Exhibit F-4

--147. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to L307 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--148. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

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wherein, in said variant, the amino acid residue at a position corresponding to F343 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--149. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID

Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to F403 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--150. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to H405 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--151. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to H406 in *Bacillus licheniformis* alpha-amylase has been substituted.--

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--152. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID
Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic
Computer Group, Version 7.0) using default values for GAP penalties, and
wherein, in said variant, the amino acid residue at a position corresponding to
D407 in *Bacillus licheniformis* alpha-amylase has been substituted.--

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--153. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID
Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic
Computer Group, Version 7.0) using default values for GAP penalties, and
wherein, in said variant, the amino acid residue at a position corresponding to
L427 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--154. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID

Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to I428 in *Bacillus licheniformis* alpha-amylase which has been substituted.--

--155. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to D430 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--156. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos: 2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, and

wherein, in said variant, the amino acid residue at a position corresponding to G433 in *Bacillus licheniformis* alpha-amylase has been substituted.--

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--157. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, or has an amino acid sequence at least 70% homologous to SEQ ID
Nos: 2, 4, 6, or 13, when homology is determined by the GAP program (Genetic
Computer Group, Version 7.0) using default values for GAP penalties, and
wherein, in said variant, the amino acid residue at a position corresponding to
G475 in *Bacillus licheniformis* alpha-amylase has been substituted.--

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--158. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and
wherein, in said variant, at least one amino acid residue at a position correspond-
ing to one or more of, Q298, G299, G301, Y302, L307, F343, F403, H405, H406,
D407, L427, I428, D430, G433, and G475 in *Bacillus licheniformis* has been
substituted.--

--159. The variant according to claim 158, wherein said alpha-amylase is
produced by *Bacillus*.--

--160. The variant according to claim 159, wherein said alpha-amylase is produced by *Bacillus licheniformis*, *Bacillus amyloliquefaciens* or *Bacillus stearothermophilus*.--

--161. A detergent comprising the variant according to claim 158.--

--162. A starch liquefaction composition comprising the variant according to claim 158.--

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--163. The variant according to claim 158, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis*.--

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--164. The variant according to claim 158, wherein said variant further comprises a substitution or deletion at one or more residue equivalent to M15, V128, H133, N188, A209, and/or M197 in *Bacillus licheniformis*.--

--165. The variant according to claim 158, wherein said variant further comprises a substitution at an amino acid residue at a position corresponding to one or more of G301, H405 and/or K436 in *Bacillus licheniformis*.--

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--166. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and
wherein, in said variant, at least one amino acid residue at a position correspond-
ing to one or more of Q298, G299, G301, Y302, L307, F343, H405, H406, D407,
I428, D430, and G475 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--167. The variant according to claim 166, wherein said alpha-amylase is
produced by *Bacillus*--

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--168. The variant according to claim 167, wherein said alpha-amylase is
produced by *Bacillus licheniformis*, *Bacillus amyloliquefaciens* or *Bacillus*
stearothermophilus--

--169. A detergent comprising the variant according to claim 166.--

--170. A starch liquefaction composition comprising the variant according to
claim 166.--

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--171. The variant according to claim 166, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, N188, A209 and/or M197 in *Bacillus licheniformis* alpha-amylase.--

--172. The variant according to claim 166, wherein said variant further comprises a substitution or deletion at one or more residues equivalent to M15, V128, H133, N188, A209, and/or M197 in *Bacillus licheniformis* alpha-amylase.--

--173. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to Q298 in *Bacillus licheniformis* alpha-amylase has been substituted.--

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--174. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to G299 in *Bacillus licheniformis* alpha-amylase has been substituted.--

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--175. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to
G301 in *Bacillus licheniformis* alpha-amylase has been substituted.--

-- 176. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to
Y302 in *Bacillus licheniformis* alpha-amylase has been substituted.--

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--177. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to
L307 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--178. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to
F343 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--179. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to
F403 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--180. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to
H405 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--181. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to H406 in *Bacillus licheniformis* alpha-amylase has been substituted.--

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--182. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to D407 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--183. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to L427 in *Bacillus licheniformis* alpha-amylase has been substituted.--
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--184. A variant of a parent alpha-amylase,
wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:
2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to I428 in *Bacillus licheniformis* alpha-amylase which has been substituted.--

--185. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:

2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to D430 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--186. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:

2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to G433 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--187. A variant of a parent alpha-amylase,

wherein said parent alpha-amylase has the amino acid sequence of SEQ ID Nos:

2, 4, 6, or 13, and

wherein, in said variant, the amino acid residue at a position corresponding to G475 in *Bacillus licheniformis* alpha-amylase has been substituted.--

--188. A variant of a parent Termamyl-like α -amylase, in which variant at least one of the amino acid residues of the parent α -amylase, which is present in a fragment

corresponding to amino acid residues 322-346 of the amino acid sequence of SEQ ID No. 2, has/have been deleted or replaced with one or more amino acid residues, which is/are present in an amino acid fragment corresponding to amino acid residues 291-313 of the amino acid sequence shown in SEQ ID No. 10, or in which one or more additional amino acid residues has/have been inserted using the relevant part of SEQ ID No. 10 or a corresponding part of another Fungamyl-like α -amylase as a template.--

--189. The variant according to claim 188, in which the amino acid fragment X-Y of the parent α -amylase, which corresponds to or is within the amino acid fragment 322-346 of SEQ ID No. 2, has/have been replaced with an amino acid fragment Z-V, which corresponds to or is within the amino acid fragment 291-313 of the amino acid sequence shown in the SEQ ID No. 10, in which variant

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X is an amino acid residue corresponding to the amino acid occupying position 322, 323, 324, or 325 of SEQ ID No.2,

Y is an amino acid residue corresponding to the amino acid occupying position 343, 344, 345 or 346 of SEQ ID No. 2, and

Z is an amino acid residue corresponding to the amino acid occupying position 291, 292, 293 or 294 of SEQ ID No. 10, and

V is an amino acid residue corresponding to the amino acid occupying position 310, 311, 312 or 313 of SEQ ID No. 10.--

--190. The variant according to claim 188, in which the amino acid fragment of the parent α -amylase, which corresponds to amino acid residues 325-345 of SEQ ID No. 2, has been replaced with the amino acid fragment corresponding to amino acid residues 294-313 of the amino acid sequence shown in SEQ ID No. 10.--

--191. The variant according to claim 189, in which the amino acid fragment of the parent α -amylase, which corresponds to amino acid residues 325-345 of SEQ ID No. 2, has been replaced with the amino acid fragment corresponding to amino acid residues 294-313 of the amino acid sequence shown in SEQ ID No. 10.--

--192. A variant of a parent α -amylase, said parent alpha-amylase having SEQ ID No. 2, in which variant the amino acid residues 325-345 of the parent α -amylase have been replaced with amino acid residues 294-313 of SEQ ID No. 10.--

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